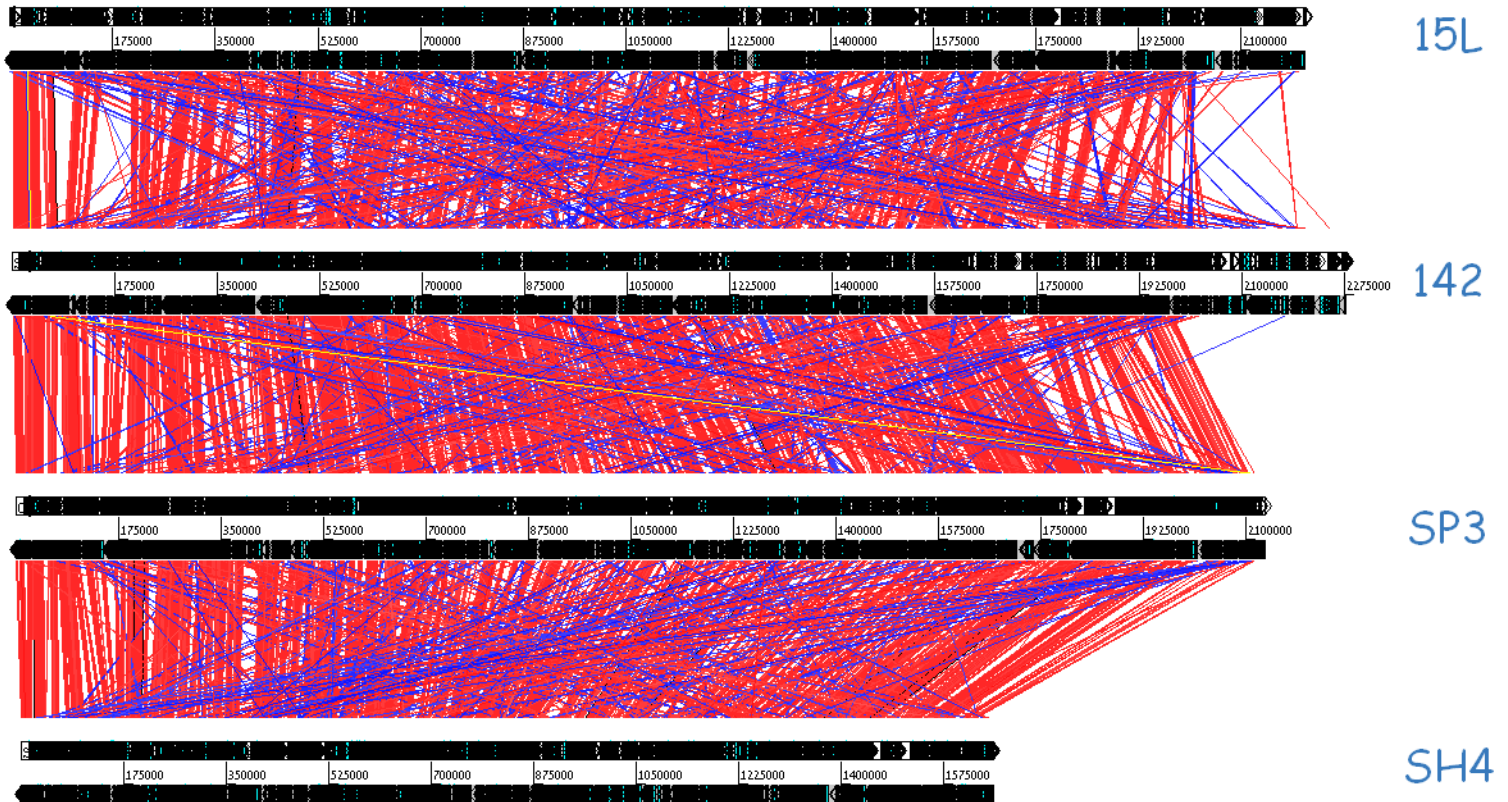


A



B

FIG S1 (A) Alignment of four "*Ca. Synechococcus spongiarum*" genomes in BRIG (84) based on BLASTp. The genomes of SH4, 142 and 15L are aligned with that of SP3, which showed the highest completeness and the fewest contigs. (B) Pairwise alignment of four draft genomes of "*Ca. Synechococcus spongiarum*" based on BLASTn. Bars indicate corresponding regions that are oriented in the same (red) and opposite (blue) directions.